

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

ggrepel

RRID:SCR_017393

Type: Tool

Proper Citation

ggrepel (RRID:SCR_017393)

Resource Information

URL: <https://cran.r-project.org/package=ggrepel>

Proper Citation: ggrepel (RRID:SCR_017393)

Description: Software tool to provide text and label geoms for ggplot2 that help to avoid overlapping text labels. Labels repel away from each other and away from data points.

Resource Type: software application, software resource, standalone software

Keywords: text, label, geoms, avoid, overlapping

Availability: Free, Available for download, Freely available

Resource Name: ggrepel

Resource ID: SCR_017393

Alternate URLs: <https://github.com/slowkow/ggrepel>

License: GNU GPL v3

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260905T133302+0000

Ratings and Alerts

No rating or validation information has been found for ggrepel.

No alerts have been found for ggrepel.

Data and Source Information

Usage and Citation Metrics

We found 63 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hassan AZ, et al. (2026) Orobas: A computational approach for scoring and analysis of quantitative chemical-genetic interactions from CRISPR-Cas9 screens. STAR protocols, 7(2), 104594.

Zambrano-Harvey AR, et al. (2026) Cancer incidence in the Pijao indigenous population of colombia using administrative health records, 1996-2022. Scientific reports, 16(1).

Zhao Y, et al. (2026) Dextrorotatory kynurenine suppresses acute rejection through inhibiting M1 macrophage-mediated inflammation. EMBO molecular medicine, 18(3), 979.

L??tsch J, et al. (2026) Voronoi tessellation as a complement or replacement for confidence ellipses in the visualization of data projection and clustering results. PloS one, 21(4), e0333653.

Orcel E, et al. (2026) UMI-guided single locus sequence typing method for phylotyping Cutibacterium acnes from skin samples. Frontiers in cellular and infection microbiology, 16, 1807759.

Menezes-Silva L, et al. (2026) Hormonal rewiring of immunity during dietary restriction ensures host defense and systemic glucose conservation. Immunity, 59(3), 700.

Tercan B, et al. (2025) Protocol for assessing distances in pathway space for classifier feature sets from machine learning methods. STAR protocols, 6(2), 103681.

Priego-Cubero S, et al. (2025) Evolution and diversification of the momilactone biosynthetic gene cluster in the genus Oryza. The New phytologist, 245(6), 2681.

de Ocampo MP, et al. (2025) Leaf Na⁺ effects and multi-trait GWAS point to salt exclusion as the key mechanism for reproductive stage salinity tolerance in rice. Annals of botany, 135(5), 949.

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. Frontiers in immunology, 16, 1572789.

Song X, et al. (2025) Leaf functional metabolic traits reveal the adaptation strategies of larch trees along the R/B ratio gradient at the stand level. Scientific reports, 15(1), 19185.

Lin CP, et al. (2025) Spatiotemporal dynamics reveal high turnover and contrasting assembly processes in fungal communities across contiguous habitats of tropical forests. Environmental microbiome, 20(1), 23.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

Wang H, et al. (2025) Phenotypic plasticity and increased infiltration of peripheral blood-derived TREM1+ mono-macrophages following radiotherapy in rectal cancer. *Cell reports. Medicine*, 6(1), 101887.

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. *Cell reports. Medicine*, 6(3), 102027.

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Chan M, et al. (2024) A kinase to cytokine explorer to identify molecular regulators and potential therapeutic opportunities. *eLife*, 12.

Hoyer MJ, et al. (2024) Combinatorial selective ER-phagy remodels the ER during neurogenesis. *Nature cell biology*, 26(3), 378.